The possibility of former biogeographic connections across the African continent between the arid regions in south western Africa and the Sahara-Sindic region has been richly debated over many years. Disjunctions in the distributions of many taxa serve as evidence for these links. It appears that in previous periods of drought, an arid corridor opened and closed a number of times. Paleoclimatic reconstructions based on polar ice cores, oceanic dust depositions and their isotopic oxygen composition now allow us to gain a much clearer picture about when and with which periodicity the arid corridor may have appeared. One way of testing a hypothesis of these linkages is through phylogenetic reconstruction within a group of plants that occurs over this range. To this end, the chloroplast *trn*LF and *rbc*L sequences of almost all southern African and a representative group of northern hemisphere species of *Zygophyllum* were obtained and used to establish a phylogeny of the genus. The clade structure in this phylogeny shows evidence of repeated migrations from southern Africa to the horn of Africa and back supporting the hypothesis of a repeated opening and closing of the arid corridor. These findings and their implications will be presented.

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## Can genomics and bioinformatics be applied to studies of non-model plants such as pearl millet?

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Pearl millet is a cereal crop important for food security in Africa and Asia. We have shown that it exhibits induced resistance to the rust fungus, *Puccinia substriata*. A generalized understanding of biochemical plant defences can be derived from studies of model plants such as *Arabidopsis thaliana* or rice, for which genome sequences are available. However, we have chosen to apply genomics and bioinformatics approaches directly to pearl millet. cDNA libraries enriched for 1920 transcripts that were differentially expressed in response to pathogen elicitors were constructed using the suppression subtractive hybridisation (SSH) technique. A quantitative method was developed to screen the SSH libraries on microarrays, and a software package SSHscreen written in R has been made publicly available (http://www.microarray.up.ac.za/SSHscreen/). Data analysis using an appropriate normalisation method indicated that the libraries were of high quality, for example 95% of the clones from the forward library represented induced transcripts, and only 5% of the clones were derived from rRNA. SSHscreen facilitates the selection of clones for DNA sequencing and reports whether induced genes are rare or abundant. The rice genome sequence was exploited by development of a web-based data mining tool termed MADIBA (*M*icroArray *D*atabase for *I*nterpretation of *B*iological *A*nnotations) to interpret the pearl millet microarray data (http://www.bi.up.ac.za/MADIBA/MADIBA.html). Induction of candidate defence genes with roles in calcium signalling and biosynthesis of signalling molecules was confirmed by quantitative Reverse Transcriptase-PCR.

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## Spatial pattern of genetic variation in *Elytropappus rhinocerotis* (Asteraceae) from the Cape provinces of South Africa

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Plant species from the unique winter-rainfall region of South Africa are likely to have changed their distributions in response to late-Quaternary changes in rainfall amount and seasonality. We used a molecular fingerprinting tool, inter-simple sequence repeat (ISSR) PCR to examine the spatial distribution of genetic variation in a shrub from an endemic lineage. Our aim was to compare the observed patterns with those expected from a hypothesised Holocene contraction in the northern part of the range. In addition, we were interested in finding areas characterised by unusual levels of genetic diversity. High-diversity areas may house older populations, indicating that they have provided long-term stable habitat for the species throughout the climatic perturbations of the Holocene ("refugia"). Low-diversity areas might indicate recent colonisation or population size reductions. We detected a large amount of genetic variation in the species, which was apportioned largely amongst individuals within populations rather than amongst populations or regions, as expected for an outcrossing and well-dispersed plant species. However, there was significant spatial structure and a very uneven distribution of diversity across the range. Geographic distance is a very poor predictor of genetic distance

between localities, especially towards the east of the range. This may be due to range alteration over the time-scale reflected by ISSR polymorphism. Inter-SSR variation declined from south to north in the western arm of the range, consistent with the prediction of Holocene aridification starting first and being most extreme in the north. Areas shown by the marker to have high levels of variability include the eastern arm of the range and the Kamiesberg highlands. Possible explanations for the observed patterns of ISSR variation are discussed.

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## To what extent are the alien plant clearing methods currently used in the Western Cape resulting in riparian ecosystem recovery?

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Invasive alien clearing has been ongoing for a number of years in South Africa and has more recently been brought to the fore by the Working for Water project. A major focus has been clearing primary catchments including riparian zones adjacent to streams. The main aims of Working for Water are to remove alien vegetation and promote natural vegetation cover, with the intention of increase surface runoff to streams. Project managers in charge of alien plant removal use various clearing methods, usually based on experience and knowledge. Past studies have provided managers with information on how best to reduce alien plant cover. However, little is known about which methods best promote natural vegetation recovery after alien clearing. This study focuses on the removal of dense alien stands cleared more than two years prior to sampling to find out which methods best promote indigenous vegetation recovery. Since only invaded and cleared sites were sampled another database dealing with pristine riparian zones was used to ascertain reference conditions. Three initial clearing treatments (fell only, fell and remove, and fell and burn) were compared to reference vegetation to answer the following questions: (1) Is there a difference between cleared plots and reference plots? (2) Do different methods of alien removal have different effects on indigenous vegetation? and (3) Are cleared plots on a trajectory towards recovery? Community parameters (composition, diversity, cover and richness) were used to test the difference in clearing methods and the results will be presented.

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## Systematic studies in the genus *Lebeckia* and related genera: A revision of *Lebeckia* section *Stiza* (Crotalarieae, Fabaceae)

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The genus *Lebeckia* consists of 36 species occurring mainly in the southern and western parts of South Africa and Namibia. Based on morphological evidence the genus does not appear to be a natural group. As part of an ongoing study on the generic circumscription of *Lebeckia*, the section *Stiza* was revised. This group is endemic to the Cape and consists of three species: *L. cuspidosa*, *L. psiloloba* and *L. pungens*. They are extremely thorny shrubs with very sparse, unifoliolate leaves and differ mainly in their reproductive morphologies (i.e. flowers, seeds, pods), pubescence and allopatric geographical distributions. The correct nomenclature, typification, distributions and diagnostic characters will be presented. The possible generic circumscriptions of those species not included in the type section of *Lebeckia* will also be discussed.

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## What limits trees in savannas? The Australian puzzle

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Savannas are characterized by lower tree biomass than forests and thickets that occur in the same landscape. Explanations for the low, and variable, tree cover include seasonal drought, low nutrient supply, competition with grasses, and the effects of fire and herbivory on tree recruitment and mortality. Australian savannas differ from other savannas in that trees increase linearly with rainfall and form relatively uniform cover within landscapes. As global outliers, Australian savannas are a challenge for hypotheses on what limits trees elsewhere. Here we report a study of determinants of tree cover in savannas in the Northern Territory. We show that eucalypts account for the difference. We compared eucalypt and non-eucalypt demography and physiology to determine potential causes of the differences. We found no evidence for differences in competition for resources, or ability to recover from fire damage. Instead the key difference lies in the remarkable growth rates of eucalypt saplings which allows them to escape the fire trap more frequently than any other tree. We discuss the physiological basis for this difference.

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